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RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/899,059

DATE: 07/24/2001

TIME: 10:41:34

Input Set : A:\PF141P7.txt

Output Set: N:\CRF3\07242001\I899059.raw

P.S

ENTERED

2 <110> APPLICANT: Yu, Guo-Liang
 3 Ni, Jian
 4 Rosen, Craig A.
 5 Zhang, Jun
 7 <120> TITLE OF INVENTION: Tumor Necrosis Factor Gamma
 9 <130> FILE REFERENCE: PF141P7
 C--> 11 <140> CURRENT APPLICATION NUMBER: US/09/899,059
 12 <141> CURRENT FILING DATE: 2001-07-06
 14 <150> PRIOR APPLICATION NUMBER: 60/278,449
 15 <151> PRIOR FILING DATE: 2001-03-26
 17 <150> PRIOR APPLICATION NUMBER: 60/216,879
 18 <151> PRIOR FILING DATE: 2000-07-07
 20 <150> PRIOR APPLICATION NUMBER: 09/559,290
 21 <151> PRIOR FILING DATE: 2000-04-27
 23 <150> PRIOR APPLICATION NUMBER: 60/180,908
 24 <151> PRIOR FILING DATE: 2000-02-08
 26 <150> PRIOR APPLICATION NUMBER: 60/134,067
 27 <151> PRIOR FILING DATE: 1999-05-13
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 33 <151> PRIOR FILING DATE: 1999-04-30
 35 <150> PRIOR APPLICATION NUMBER: 09/246,129
 36 <151> PRIOR FILING DATE: 1999-02-08
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 44 <150> PRIOR APPLICATION NUMBER: 09/005,020
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 48 <151> PRIOR FILING DATE: 1995-06-05
 50 <150> PRIOR APPLICATION NUMBER: PCT/US94/12880
 51 <151> PRIOR FILING DATE: 1994-11-07
 53 <160> NUMBER OF SEQ ID NOS: 30
 55 <170> SOFTWARE: PatentIn Ver. 2.0
 57 <210> SEQ ID NO: 1
 58 <211> LENGTH: 2442
 59 <212> TYPE: DNA
 60 <213> ORGANISM: Homo sapiens
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 63 <221> NAME/KEY: CDS
 64 <222> LOCATION: (783)..(1304)
 66 <220> FEATURE:
 67 <221> NAME/KEY: mat_peptide
 68 <222> LOCATION: (864)..(1304)
 70 <220> FEATURE:

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72 <222> LOCATION: (783)..(863)
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75 <221> NAME/KEY: misc_feature
76 <222> LOCATION: (2265)
77 <223> OTHER INFORMATION: n equals a, t, g, or c
79 <220> FEATURE:
80 <221> NAME/KEY: misc_feature
81 <222> LOCATION: (2273)
82 <223> OTHER INFORMATION: n equals a, t, g, or c
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85 <221> NAME/KEY: misc_feature
86 <222> LOCATION: (2307)
87 <223> OTHER INFORMATION: n equals a, t, g, or c
89 <220> FEATURE:
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91 <222> LOCATION: (2336)
92 <223> OTHER INFORMATION: n equals a, t, g, or c
94 <220> FEATURE:
95 <221> NAME/KEY: misc_feature
96 <222> LOCATION: (2341)
97 <223> OTHER INFORMATION: n equals a, t, g, or c
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101 <222> LOCATION: (2379)
102 <223> OTHER INFORMATION: n equals a, t, g, or c
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105 cccaatcaag agaaattcca tactatcacc agttggccga ctttccaagt ctagtgcaga 60
107 aatccaaggc acctcacacc tagagttcct atacctctga gactccagag gaaagaacaa 120
109 gacagtgagc aaggatatgt tagaaccacac tgaaaacctga gaaggttgaa aaggaagcat 180
111 accctcctga cctataagaa aattttcagt ctgcaggggg atatccttgt ggcccaagac 240
113 attggtgtta tcatttgact aagaggaaat tatttggtgt gagctctgag tgaggattag 300
115 gaccagggag atgccaagtt tctatcactt acctcatgcc tgtaagacaa gtgttttgtt 360
117 ccaattgatg aatggggaga aaacagttca gccaatcact tatgggcaca gaatggaatt 420
119 tgaagggtct ggtgcctgcc ctgtgcatac gtaaacaaga gaggcacgag tgagttttat 480
121 ctgagtcatt tgggaaagga taattcttgc accaagccat tttcctaaac acagaagaat 540
123 aggggggattc cttaaccttc attgttctcc aggatcatag gtctcaggat aaattaaaaa 600
125 ttttcagggtc agaccactca gtctcagaaa ggcaaagtaa tttgccccag gtcactagtc 660
127 caagatgtta ttctctttga acaaattgtgt atgtccagtc acatattctt cattcattcc 720
129 tccccaaagc agtttttagc tgttaggtat attcgatcac tttagttctat tttgaaaatg 780
131 at atg aga cgc ttt tta agc aaa gtc tac agt ttc cca atg aga aaa 827
132 Met Arg Arg Phe Leu Ser Lys Val Tyr Ser Phe Pro Met Arg Lys
133 -25 -20 -15
135 tta atc ctc ttt ctt gtc ttt cca gtt gtg aga caa act ccc aca cag 875
136 Leu Ile Leu Phe Leu Val Phe Pro Val Val Arg Gln Thr Pro Thr Gln
137 -10 -5 -1 1
139 cac ttt aaa aat cag ttc cca gct ctg cac tgg gaa cat gaa cta ggc 923
140 His Phe Lys Asn Gln Phe Pro Ala Leu His Trp Glu His Glu Leu Gly
141 5 10 15 20

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143 ctg gcc ttc acc aag aac cga atg aac tat acc aac aaa ttc ctg ctg 971
144 Leu Ala Phe Thr Lys Asn Arg Met Asn Tyr Thr Asn Lys Phe Leu Leu
145          25          30          35
147 atc cca gag tgc gga gac tac ttc att tac tcc cag gtc aca ttc cgt 1019
148 Ile Pro Glu Ser Gly Asp Tyr Phe Ile Tyr Ser Gln Val Thr Phe Arg
149          40          45          50
151 ggg atg acc tct gag tgc agt gaa atc aga caa gca ggc cga cca aac 1067
152 Gly Met Thr Ser Glu Cys Ser Glu Ile Arg Gln Ala Gly Arg Pro Asn
153          55          60          65
155 aag cca gac tcc atc act gtg gtc atc acc aag gta aca gac agc tac 1115
156 Lys Pro Asp Ser Ile Thr Val Val Ile Thr Lys Val Thr Asp Ser Tyr
157          70          75          80
159 cct gag cca acc cag ctc ctc atg ggg acc aag tct gta tgc gaa gta 1163
160 Pro Glu Pro Thr Gln Leu Leu Met Gly Thr Lys Ser Val Cys Glu Val
161 85          90          95          100
163 ggt agc aac tgg ttc cag ccc atc tac ctc gga gcc atg ttc tcc ttg 1211
164 Gly Ser Asn Trp Phe Gln Pro Ile Tyr Leu Gly Ala Met Phe Ser Leu
165          105          110          115
167 caa gaa ggg gac aag cta atg gtg aac gtc agt gac atc tct ttg gtg 1259
168 Gln Glu Gly Asp Lys Leu Met Val Asn Val Ser Asp Ile Ser Leu Val
169          120          125          130
171 gat tac aca aaa gaa gat aaa acc ttc ttt gga gcc ttc tta cta 1304
172 Asp Tyr Thr Lys Glu Asp Lys Thr Phe Phe Gly Ala Phe Leu Leu
173          135          140          145
175 taggaggaga gcaaatatca ttatatgaaa gtcctctgcc accgagttcc taattttctt 1364
177 tgttcaaatg taattataac caggggtttt cttggggccg ggagtagggg gcattccaca 1424
179 gggacaacgg tttagctatg aaatttgggg ccaaaatttc acacttcatg tgccttactg 1484
181 atgagagtac taactggaaa aaggctgaag agagcaataa tattattaag atgggttgga 1544
183 ggattggcga gtttctaaat attagacac tgatcactaa atgaatggat gatctactcg 1604
185 ggtcaggatt gaaagagaaa tatttcaaca cctccctgct atacaatggg caccagtggg 1664
187 ccagttattg ttcaatttga tcataaattt gcttcaattc aggagctttg aagggaagtcc 1724
189 aaggaaagct ctagaaaaca gtataaactt tcagaggcaa aatccttcac caatttttcc 1784
191 acatactttc atgccttgcc taaaaaaaat gaaaagagag ttggtatgtc tcatgaatgt 1844
193 tcacacagaa ggagttgggt ttcattgtcat ctacagcata tgagaaaagc tacctttctt 1904
195 ttgattatgt acacagatat ctataaagg aagtttgagt ttcacatgta tatcccaaat 1964
197 acaacagttg cttgtattca gtagagtttt cttgccacc tattttgtgc tgggttctac 2024
199 ctaacccag aagacactat gaaaaacaag acagactcca ctcaaaattt atatgaacac 2084
201 cactagatac ttctgatca aacatcagtc aacatactct aaagaataac tccaagtctt 2144
203 ggccaggcgc agtggctcac acctgtaate ccaacacttt gggaggccaa ggtgggtgga 2204
205 tcatctaagg ccgggagttc aagaccagcc tgaccaacgt ggagaaaccc catctctact 2264
207 naaaatacna aattagcgg gcgtggtagc gcatggctgt aancctggct actcaggagg 2324
W-→ 209 ccgaggcaga anaattnctt gaactgggga ggcagaggtt gcggtgagcc caganccgcgc 2384
211 cattgcactc cagcctgggt aacaagagca aaactctgtc caaaaaaaaa aaaaaaaaa 2442
213 <210> SEQ ID NO: 2
214 <211> LENGTH: 174
215 <212> TYPE: PRT
216 <213> ORGANISM: Homo sapiens
218 <400> SEQUENCE: 2
219 Met Arg Arg Phe Leu Ser Lys Val Tyr Ser Phe Pro Met Arg Lys Leu

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220          -25          -20          -15
222 Ile Leu Phe Leu Val Phe Pro Val Val Arg Gln Thr Pro Thr Gln His
223          -10          -5          -1 1 5
225 Phe Lys Asn Gln Phe Pro Ala Leu His Trp Glu His Glu Leu Gly Leu
226          10          15          20
228 Ala Phe Thr Lys Asn Arg Met Asn Tyr Thr Asn Lys Phe Leu Leu Ile
229          25          30          35
231 Pro Glu Ser Gly Asp Tyr Phe Ile Tyr Ser Gln Val Thr Phe Arg Gly
232          40          45          50
234 Met Thr Ser Glu Cys Ser Glu Ile Arg Gln Ala Gly Arg Pro Asn Lys
235          55          60          65
237 Pro Asp Ser Ile Thr Val Val Ile Thr Lys Val Thr Asp Ser Tyr Pro
238          70          75          80          85
240 Glu Pro Thr Gln Leu Leu Met Gly Thr Lys Ser Val Cys Glu Val Gly
241          90          95          100
243 Ser Asn Trp Phe Gln Pro Ile Tyr Leu Gly Ala Met Phe Ser Leu Gln
244          105          110          115
246 Glu Gly Asp Lys Leu Met Val Asn Val Ser Asp Ile Ser Leu Val Asp
247          120          125          130
249 Tyr Thr Lys Glu Asp Lys Thr Phe Phe Gly Ala Phe Leu Leu
250          135          140          145
252 <210> SEQ ID NO: 3
253 <211> LENGTH: 233
254 <212> TYPE: PRT
255 <213> ORGANISM: Homo sapiens
257 <400> SEQUENCE: 3
258 Met Ser Thr Glu Ser Met Ile Arg Asp Val Glu Leu Ala Glu Glu Ala
259 1 5 10 15
261 Leu Pro Lys Lys Thr Gly Gly Pro Gln Gly Ser Arg Arg Cys Leu Phe
262 20 25 30
264 Leu Ser Leu Phe Ser Phe Leu Ile Val Ala Gly Ala Thr Thr Leu Phe
265 35 40 45
267 Cys Leu Leu His Phe Gly Val Ile Gly Pro Gln Arg Glu Glu Ser Pro
268 50 55 60
270 Arg Asp Leu Ser Leu Ile Ser Pro Leu Ala Gln Ala Val Arg Ser Ser
271 65 70 75 80
273 Ser Arg Thr Pro Ser Asp Lys Pro Val Ala His Val Val Ala Asn Pro
274 85 90 95
276 Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu
277 100 105 110
279 Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln Leu Val Val Pro Ser
280 115 120 125
282 Glu Gly Leu Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly
283 130 135 140
285 Cys Pro Ser Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala
286 145 150 155 160
288 Val Ser Tyr Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro
289 165 170 175
291 Cys Gln Arg Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu

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292          180          185          190
294 Pro Ile Tyr Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu
295          195          200          205
297 Ser Ala Glu Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly
298          210          215          220
300 Gln Val Tyr Phe Gly Ile Ile Ala Leu
301 225          230
303 <210> SEQ ID NO: 4
304 <211> LENGTH: 205
305 <212> TYPE: PRT
306 <213> ORGANISM: Homo sapiens
308 <400> SEQUENCE: 4
309 Met Thr Pro Pro Glu Arg Leu Phe Leu Pro Arg Val Cys Gly Thr Thr
310 1          5          10          15
312 Leu His Leu Leu Leu Leu Gly Leu Leu Leu Val Leu Leu Pro Gly Ala
313          20          25          30
315 Gln Gly Leu Pro Gly Val Gly Leu Thr Pro Ser Ala Ala Gln Thr Ala
316          35          40          45
318 Arg Gln His Pro Lys Met His Leu Ala His Ser Thr Leu Lys Pro Ala
319          50          55          60
321 Ala His Leu Ile Gly Asp Pro Ser Lys Gln Asn Ser Leu Leu Trp Arg
322 65          70          75          80
324 Ala Asn Thr Asp Arg Ala Phe Leu Gln Asp Gly Phe Ser Leu Ser Asn
325          85          90          95
327 Asn Ser Leu Leu Val Pro Thr Ser Gly Ile Tyr Phe Val Tyr Ser Gln
328          100          105          110
330 Val Val Phe Ser Gly Lys Ala Tyr Ser Pro Lys Ala Pro Ser Ser Pro
331          115          120          125
333 Leu Tyr Leu Ala His Glu Val Gln Leu Phe Ser Ser Gln Tyr Pro Phe
334          130          135          140
336 His Val Pro Leu Leu Ser Ser Gln Lys Met Val Tyr Pro Gly Leu Gln
337 145          150          155          160
339 Glu Pro Trp Leu His Ser Met Tyr His Gly Ala Ala Phe Gln Leu Thr
340          165          170          175
342 Gln Gly Asp Gln Leu Ser Thr His Thr Asp Gly Ile Pro His Leu Val
343          180          185          190
345 Leu Ser Pro Ser Thr Val Phe Phe Gly Ala Phe Ala Leu
346          195          200          205
348 <210> SEQ ID NO: 5
349 <211> LENGTH: 244
350 <212> TYPE: PRT
351 <213> ORGANISM: Homo sapiens
353 <400> SEQUENCE: 5
354 Met Gly Ala Leu Gly Leu Glu Gly Arg Gly Gly Arg Leu Gln Gly Arg
355 1          5          10          15
357 Gly Ser Leu Leu Leu Ala Val Ala Gly Ala Thr Ser Leu Val Thr Leu
358          20          25          30
360 Leu Leu Ala Val Pro Ile Thr Val Leu Ala Val Leu Ala Leu Val Pro
361          35          40          45

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Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

VERIFICATION SUMMARY

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L:11 M:270 C: Current Application Number differs, Replaced Current Application Number

L:207 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:209 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1
L:545 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:549 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:557 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:559 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:8
L:665 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:667 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:669 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:671 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:673 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:9
L:716 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:724 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:726 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:728 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10
L:786 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:788 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:796 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:798 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:800 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11
L:878 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:880 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:882 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:884 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
L:886 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:12
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L:1113 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1121 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1123 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
L:1256 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1258 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1262 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1264 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1266 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1268 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:22
L:1346 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1348 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1350 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1352 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1354 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1356 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1358 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:23
L:1416 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1418 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24
L:1426 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:24

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